

SEQUENCE LISTING

<110> Bayer CropScience Aktiengesellschaft

<120> Helicokinin receptor

<130> Le A 36 033

<160> 2

<170> PatentIn version 3.1

<210> 1

<211> 1452

<212> DNA

<213> Heliothis virescens

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<221> CDS

<222> (1) .. (1452)

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1				5					10					15		

cca	agg	aac	agt	tcc	att	gac	gag	tat	att	ata	cac	aat	gga	act	aat	96
Pro	Arg	Asn	Ser	Ser	Ile	Asp	Glu	Tyr	Ile	Ile	His	Asn	Gly	Thr	Asn	
			20					25					30			

gat	aca	ttc	gaa	aca	ttg	tac	gat	gtg	ccg	act	ggt	atg	ata	gta	ctc	144
Asp	Thr	Phe	Glu	Thr	Leu	Tyr	Asp	Val	Pro	Thr	Gly	Met	Ile	Val	Leu	
		35					40					45				

ttg	tcg	ttc	ctg	tac	ggc	tca	ata	tca	gtt	ctt	gac	gtg	gtg	ggg	aac	192
Leu	Ser	Phe	Leu	Tyr	Gly	Ser	Ile	Ser	Val	Leu	Ala	Val	Val	Gly	Asn	
	50				55						60					

ttt	ctg	gtg	atg	tgg	gtc	gtg	gcc	acc	tcg	aga	aga	atg	cag	agc	gtc	240
Phe	Leu	Val	Met	Trp	Val	Val	Ala	Thr	Ser	Arg	Arg	Met	Gln	Ser	Val	
65					70				75						80	

aca	aac	tgc	tac	ata	gcc	aac	tta	gct	tta	gct	gac	ata	gtc	ata	gga	288
Thr	Asn	Cys	Tyr	Ile	Ala	Asn	Leu	Ala	Leu	Ala	Asp	Ile	Val	Ile	Gly	
			85					90					95			

tta	ttc	gct	gta	cca	ttt	caa	ttt	caa	gcc	gac	ctg	cta	cag	cgg	tgg	336
Leu	Phe	Ala	Val	Pro	Phe	Gln	Phe	Gln	Ala	Ala	Leu	Leu	Gln	Arg	Trp	
			100					105					110			

ctg	cta	ccg	cac	ttc	atg	tgt	ccg	ttc	tgc	ccg	ttc	gtg	cag	gac	ctc	384
Leu	Leu	Pro	His	Phe	Met	Cys	Pro	Phe	Cys	Pro	Phe	Val	Gln	Ala	Leu	
		115					120					125				

agt	gtc	aac	gtc	agc	gtg	ttt	aca	ctg	aca	gcc	atc	gca	gtt	gac	aga	432
Ser	Val	Asn	Val	Ser	Val	Phe	Thr	Leu	Thr	Ala	Ile	Ala	Val	Asp	Arg	
	130					135					140					

cat	cgg	gac	ata	atc	aca	ccg	ctc	agc	gcc	cac	act	tca	aag	cgt	att	480
His	Arg	Ala	Ile	Ile	Thr	Pro	Leu	Ser	Ala	His	Thr	Ser	Lys	Arg	Ile	
145					150				155						160	

gcc	aaa	gta	ata	ata	gtg	gtt	ata	tgg	ttt	ctg	gac	ctt	tct	tta	gct	528
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Ala	Lys	Val	Ile	Ile	Val	Val	Ile	Trp	Phe	Leu	Ala	Leu	Ser	Leu	Ala		
				165					170					175			
gct	ccg	atg	gct	atg	tct	tgg	gag	gtt	atc	atg	gaa	gat	gaa	tta	gat		576
Ala	Pro	Met	Ala	Met	Ser	Trp	Glu	Val	Ile	Met	Glu	Asp	Glu	Leu	Asp		
			180					185					190				
cca	gtt	gca	aaa	atc	ttc	tac	aaa	aag	ccg	ttt	tgt	gca	ccc	acc	gag		624
Pro	Val	Ala	Lys	Ile	Phe	Tyr	Lys	Lys	Pro	Phe	Cys	Ala	Pro	Thr	Glu		
			195				200					205					
ttc	ggc	tcg	cat	tca	ctc	gcc	att	tat	aga	ctg	ttg	ttg	tat	gta	ttt		672
Phe	Gly	Ser	His	Ser	Leu	Ala	Ile	Tyr	Arg	Leu	Leu	Leu	Tyr	Val	Phe		
	210					215					220						
cag	tat	gta	atc	ccg	ttg	tgt	gtg	att	acg	ttt	gcc	tac	gct	cat	atg		720
Gln	Tyr	Val	Ile	Pro	Leu	Cys	Val	Ile	Thr	Phe	Ala	Tyr	Ala	His	Met		
	225				230				235						240		
gcg	atg	aag	ctg	tgg	gga	gcg	cgc	gcc	cca	ggg	aac	gcg	cag	gag	acg		768
Ala	Met	Lys	Leu	Trp	Gly	Ala	Arg	Ala	Pro	Gly	Asn	Ala	Gln	Glu	Thr		
				245				250						255			
agg	gac	gct	aac	cac	atg	cga	aac	aag	aag	aag	gtg	ata	aaa	atg	ttg		816
Arg	Asp	Ala	Asn	His	Met	Arg	Asn	Lys	Lys	Lys	Val	Ile	Lys	Met	Leu		
			260				265					270					
gtg	ctg	gtc	gta	gct	ctg	ttt	gcg	tta	tgc	tgg	ctg	ccg	cta	cag	agc		864
Val	Leu	Val	Val	Ala	Leu	Phe	Ala	Leu	Cys	Trp	Leu	Pro	Leu	Gln	Ser		
		275					280					285					
tac	tta	tta	cta	caa	tca	ttt	ttt	cca	tca	att	aac	gag	tac	aag	tac		912
Tyr	Leu	Leu	Leu	Gln	Ser	Phe	Phe	Pro	Ser	Ile	Asn	Glu	Tyr	Lys	Tyr		
	290					295					300						
atc	aac	gtg	ctt	ttc	ttt	tgc	ttc	gac	tgg	cta	gca	atg	agc	aac	tct		960
Ile	Asn	Val	Leu	Phe	Phe	Cys	Phe	Asp	Trp	Leu	Ala	Met	Ser	Asn	Ser		
	305				310				315						320		
tgc	tat	aac	cca	ttc	atc	tat	gcc	atc	tac	aac	gaa	aaa	ttc	aag	aag		1008
Cys	Tyr	Asn	Pro	Phe	Ile	Tyr	Ala	Ile	Tyr	Asn	Glu	Lys	Phe	Lys	Lys		
				325					330					335			
gaa	ttc	aaa	caa	cga	ttc	act	ttc	ggg	aaa	aag	cca	agc	aga	ttc	gtt		1056
Glu	Phe	Lys	Gln	Arg	Phe	Thr	Phe	Gly	Lys	Lys	Pro	Ser	Arg	Phe	Val		
			340					345					350				
aac	gat	agc	tac	gag	gac	ggc	cag	tca	tac	cga	aca	aga	att	tta	tcg		1104
Asn	Asp	Ser	Tyr	Glu	Asp	Gly	Gln	Ser	Tyr	Arg	Thr	Arg	Ile	Leu	Ser		
			355				360					365					
ttc	cga	tca	acc	aac	gac	aga	agt	ggc	tat	tca	tcc	aga	aag	tct	ttg		1152
Phe	Arg	Ser	Thr	Asn	Asp	Arg	Ser	Gly	Tyr	Ser	Ser	Arg	Lys	Ser	Leu		
	370					375					380						
aac	ata	ccg	ccg	ggg	gac	act	tta	aaa	gtt	cct	tct	aga	aat	tca	tgt		1200
Asn	Ile	Pro	Pro	Gly	Asp	Thr	Leu	Lys	Val	Pro	Ser	Arg	Asn	Ser	Cys		
					390					395					400		
cat	tgc	atg	gcg	aat	cag	agc	aga	gaa	aat	gga	ttt	aac	ttc	atg	aaa		1248
His	Cys	Met	Ala	Asn	Gln	Ser	Arg	Glu	Asn	Gly	Phe	Asn	Phe	Met	Lys		
				405					410					415			
act	gaa	gac	atg	gaa	ggg	cac	gga	aat	agc	agg	cgg	tat	ctg	aat	ata		1296
Thr	Glu	Asp	Met	Glu	Gly	His	Gly	Asn	Ser	Arg	Arg	Tyr	Leu	Asn	Ile		

420										425					430					
aga	atg	agt	aat	cca	gat	att	ggg	aaa	aga	aga	tta	gct	aag	aag	tta	1344				
Arg	Met	Ser	Asn	Pro	Asp	Ile	Gly	Lys	Arg	Arg	Leu	Ala	Lys	Lys	Leu					
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tcg	aat	aga	gac	gac	atg	cct	ata	ggg	gat	gag	aga	gtc	agt	gaa	ctg	1392				
Ser	Asn	Arg	Asp	Asp	Met	Pro	Ile	Gly	Asp	Glu	Arg	Val	Ser	Glu	Leu					
	450					455					460									
tac	ata	ttc	cca	aac	agt	aac	att	gta	gaa	ttt	aca	gac	ata	tca	tac	1440				
Tyr	Ile	Phe	Pro	Asn	Ser	Asn	Ile	Val	Glu	Phe	Thr	Asp	Ile	Ser	Tyr					
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gat	gac	aaa	gtg													1452				
Asp	Asp	Lys	Val																	

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			20					25					30			
Asp	Thr	Phe	Glu	Thr	Leu	Tyr	Asp	Val	Pro	Thr	Gly	Met	Ile	Val	Leu	
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Leu	Ser	Phe	Leu	Tyr	Gly	Ser	Ile	Ser	Val	Leu	Ala	Val	Val	Gly	Asn	
	50					55					60					
Phe	Leu	Val	Met	Trp	Val	Val	Ala	Thr	Ser	Arg	Arg	Met	Gln	Ser	Val	
65					70				75						80	
Thr	Asn	Cys	Tyr	Ile	Ala	Asn	Leu	Ala	Leu	Ala	Asp	Ile	Val	Ile	Gly	
				85				90						95		
Leu	Phe	Ala	Val	Pro	Phe	Gln	Phe	Gln	Ala	Ala	Leu	Leu	Gln	Arg	Trp	
			100					105					110			
Leu	Leu	Pro	His	Phe	Met	Cys	Pro	Phe	Cys	Pro	Phe	Val	Gln	Ala	Leu	
		115					120					125				
Ser	Val	Asn	Val	Ser	Val	Phe	Thr	Leu	Thr	Ala	Ile	Ala	Val	Asp	Arg	
		130				135					140					
His	Arg	Ala	Ile	Ile	Thr	Pro	Leu	Ser	Ala	His	Thr	Ser	Lys	Arg	Ile	
145					150					155					160	

Ala Lys Val Ile Ile Val Val Ile Trp Phe Leu Ala Leu Ser Leu Ala
 165 170 175

Ala Pro Met Ala Met Ser Trp Glu Val Ile Met Glu Asp Glu Leu Asp
 180 185 190

Pro Val Ala Lys Ile Phe Tyr Lys Lys Pro Phe Cys Ala Pro Thr Glu
 195 200 205

Phe Gly Ser His Ser Leu Ala Ile Tyr Arg Leu Leu Leu Tyr Val Phe
 210 215 220

Gln Tyr Val Ile Pro Leu Cys Val Ile Thr Phe Ala Tyr Ala His Met
 225 230 235 240

Ala Met Lys Leu Trp Gly Ala Arg Ala Pro Gly Asn Ala Gln Glu Thr
 245 250 255

Arg Asp Ala Asn His Met Arg Asn Lys Lys Lys Val Ile Lys Met Leu
 260 265 270

Val Leu Val Val Ala Leu Phe Ala Leu Cys Trp Leu Pro Leu Gln Ser
 275 280 285

Tyr Leu Leu Leu Gln Ser Phe Phe Pro Ser Ile Asn Glu Tyr Lys Tyr
 290 295 300

Ile Asn Val Leu Phe Phe Cys Phe Asp Trp Leu Ala Met Ser Asn Ser
 305 310 315 320

Cys Tyr Asn Pro Phe Ile Tyr Ala Ile Tyr Asn Glu Lys Phe Lys Lys
 325 330 335

Glu Phe Lys Gln Arg Phe Thr Phe Gly Lys Lys Pro Ser Arg Phe Val
 340 345 350

Asn Asp Ser Tyr Glu Asp Gly Gln Ser Tyr Arg Thr Arg Ile Leu Ser
 355 360 365

Phe Arg Ser Thr Asn Asp Arg Ser Gly Tyr Ser Ser Arg Lys Ser Leu
 370 375 380

Asn Ile Pro Pro Gly Asp Thr Leu Lys Val Pro Ser Arg Asn Ser Cys
 385 390 395 400

His Cys Met Ala Asn Gln Ser Arg Glu Asn Gly Phe Asn Phe Met Lys
 405 410 415

Thr Glu Asp Met Glu Gly His Gly Asn Ser Arg Arg Tyr Leu Asn Ile
420 425 430

Arg Met Ser Asn Pro Asp Ile Gly Lys Arg Arg Leu Ala Lys Lys Leu
435 440 445

Ser Asn Arg Asp Asp Met Pro Ile Gly Asp Glu Arg Val Ser Glu Leu
450 455 460

Tyr Ile Phe Pro Asn Ser Asn Ile Val Glu Phe Thr Asp Ile Ser Tyr
465 470 475 480

Asp Asp Lys Val